

FIGURE 1

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTTCGATTTCTGTTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGGAGCGGCCCGCGCTGCTGGGCGAGCGCAGGAGCGGGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCGACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAAGTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

FIGURE 2

Query: 170 TGGCGCACCTGCACGGCATCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229
 ||| || | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCACT 61

 Query: 230 TGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA 289
 | | ||| | | | | | | | | | | | | | | | | | | | |
 Sbjct: 62 TAGAAATCTTCCCCAATGGTACTATCCAGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

 Query: 290 TCTTGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
 | | ||||| | | | | | | | | | | | | | | | | | | |
 Sbjct: 122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC 181

 Query: 350 TCTATCTTGAATGAATGACAAAGGAGAAGTCTATGGATCAGAGAACTTACTTCCGAAT 409
 | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

 Query: 410 GCATCTTTAGGGAGCAGTTTGAAGAGAAGTGGTATAACACCTATTCATCTAACATATATA 469
 | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 242 GTGTATTCAGAGAACAGTTCGAAGAAAAGTGGTATAATACGTACTCGTCAAACCTATATA 301

 Query: 470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCAAGAG 529
 | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 302 AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

 Query: 530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
 | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

 Query: 590 CAGA 593
 | | |
 Sbjct: 422 CCGA 425

FIGURE 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCTCTGCCGCGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTCTGCCGCGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCCGTGCGGCAATAGAGCTGCCGGCGGGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 15987 GGTGGAAGCCCGTGCGGCAATAGAGCTGCCGGCGG-CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGCGCGCGCGCGCGCTCCGCTCCGCGCGCGCTCCTGCGCTCGCCCA 110
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16046 GCTGCGCAGCCCCCGCGCGCGCGCGCGCTCCGCTCCGCGCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGCGCGCGCGCTCCCGCGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGCGCCA 50
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16106 GCAGCGCGCGCGCGCTCCCGCGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGCGCCA 16165

Query:    49 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTGGGCTAAGGGAGCCAT 1
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCCGACTTGGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCTCTGTACAATTCTGGAACTCTTTCTGGATCCACTGGTCTAGG 574
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7257 AGTGATACATCAGTAGGTCTCTGTACAATTCTGGAACTCTTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAAGAAATGTGTAAATTTCTGATGCTCTTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 514
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7317 TAAAGAAATGTGTAAATTTCTGATGCTCTTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 7376

Query:   513 TTTGTAAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7377 TTTGTAAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACCAATTTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7437 ATAGGTGTTATACCAATTTCTCTTCAAACCTGCTCCCTAAAGATGCATTTCGGAAGTAAGTTT 7496
```

FIGURE 3 (cont.)

Query: 393 CTC-TGATCCATAGA 380
 ||| ||| | |||
 Sbjct: 7497 CTCCTGAAAGAGAGA 7511

C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
 Identities = 106/106 (100%), Positives = 106/106 (100%),
 Strand = Minus / Plus

Query: 391 CTGATCCATAGAGTTCTCCTTTGTCATTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query: 331 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 286
 ||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 9897 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 9942

FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGE-CX (EAA93474Xen; Xenopus laevis XFGE CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

```
M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S A P - - S D L S H
M A P L A E V G G F L G G L E G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A E R S A R - G G P G A A Q L A H
```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

```
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q Q D H S R F G I L E F I S V A I G L V S I R G V D T G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L
```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

```
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N D K G E L F G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y F V A L N K D G T P R D G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N I Y K H G D T G R R Y F V A L N K D G T P R D G A
```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGE-CX

FGF-CX

```
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P D K V P E L Y K D L M G Y S
R S K R H Q K F T H F L P R P V D P D E R V P E L Y K D L L M Y T
```

FIGURE 5

FGF-CX	MAPLAEVGGFLGGLEGLGQQVGSFHLLPPAGERPPLGERRSAAERSARGGPGAAQLAH	59
XFGF-20	MAPLADVGTFLGGYDALGQVGSFHLLPPAKDSPLFNDPLAQSERLSR-SAP--SDLSH	56
FGF-9	MAPLGEVGNVFGVQDAVP--FENVPVLP--VDSPVLLSDHLGQSEAGGLPRGPAVTDLDH	56
FGF-CX ₁₋₁₆	--MAEVGGVFASLDWDLHGFSLSLGNVPLADSPGFLNERLGQIEGKLQRGSP--TDFAH	55
FGF-20	LHGILRRRQLYCRTGTFHLQILPDGSVQGTRODHSLEFGILEFISVAVGLVSIRGVDSGLYL	119
XFGF-20	LQGILRRRQLYCRTGTFHLQILPDGNVQGTRODHSRFGILEFISVALGLVSIRGVDTGLYL	116
FGF-9	LKGI LRRRQLYCRTGTFHLEIFPNGTIQGTREKDSRFGILEFISLAVGLVSIRGVDSGLYL	116
FGF-16	LKGI LRRRQLYCRTGTFHLEIFPNGTVHGTRHDHSRFGILEFISLAVGLISIRGVDSGLYL	115
FGF-20	GMNDKGLYGSSEKLTSECIFFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTPRDGA	179
XFGF-20	GMNDKGLFEGSEKLTSECIFFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGT	176
FGF-9	GMNEKGELYGSEKLTQECVFFREQFEENWYNTYSSNLYKHVDTGRRYFVALNKDGTPREGT	176
FGF-CX ₁₋₁₆	GMNERGELYGSKKLTRECFFREQFEENWYNTYASTLYKHSDSERQYFVALNKDGSFREGY	175
FGF-20	RSKRHKQKFTHFLPRPVDPERWPELYKDLLMYT	211
XFGF-20	RAKRHKQKFTHFLPRPVDPEKVPELYKDLLMGYS	208
FGF-9	RTKRHKQKFTHFLPRPVDPDKVPELYKDLLSQS	208
FGF-16	RTKRHKQKFTHFLPRPVDPSKLPSMSRDLFHYR	207

FIGURE 6

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

```

Query:      1  MAPLAEVGGFLGGLEGLGQQVGSFHLPPAGERPPLLCGERRSAAERSARG - GPGAAQLAH  59
           ||| ||| + | + + + + + + + + + + + + + + + + + + + + + + + +
Sbjct:      1  MAPLGEVGNVFGVQDAV -- PFCNVPLPV -- DSPVLLSDHLGQSEAGGLPRGPVAVTDLDH  56

Query:     60  LHGILRRRLQLYCRTGFHLQILPDGSVQGTRODHSILFGILEFISVAVGLVSIrgVDSGLYL  119
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     57  LKGILRRRLQLYCRTGFHLEIFPNGTIQGTRKDHRSFGILEFISIAVGLVSIrgVDSGLYL  116

Query:    120  GMNDKGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA  179
           ||| + ||| ||| ||| + ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| + ||
Sbjct:    117  GMNEKGELYGSEKLTQECVFREQFEENWNTYSSNLYKHVDTGRRYYVALNKDGTPREGT  176

Query:    180  RSKRHQKFTTHFLPRPVDPERVPELYKDLL  208
           | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | + |
Sbjct:    177  RTKRHQKFTTHFLPRPVPDPKVPPELYKDIL  205

```

FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%) Frame = +1

```

Query:      1  MAPLAEVGGFLGLEGLGQQVGSHFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH  59
          ||||| + | + + | + + || + || + || + + | || || || ||
Sbjct:      1  MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLLNDHLGQSEAGGLPRGPVATDLDH  56

Query:     60  LHGILRRRLQYCRGTGFHLQILPDGSVQCTRQDHSLSFGILEFISVAVGLVSIRGVDSGLYL  119
          | ||||| ||||| ||||| + | + + ||||| + ||||| ||||| ||||| |||||
Sbjct:     57  LKGILRRRLQYCRGTGFHLEIFPNGTIQGTRKDHSRFGILEFISVAVGLVSIRGVDSGLYL  116

Query:    120  GMNDKGELYGSEKLTSECTFPEQFEENWNTYSSNIYKHGDTGRRIFVALNKDGTPRDGA  179
          ||| + ||||| ||||| || + ||||| ||||| ||||| + ||||| ||||| + |
Sbjct:    117  GMNEKGELYGSEKLTQECVFREQFEENWNTYSSNLYKHVDTGRRYYVALNKDGTTPREGT  176

Query:    180  RSKRHQKFTHFLPRPVDPERVPELYKDLL  208
          | + ||||| ||||| ||||| + ||||| ||||| + ||
Sbjct:    177  RTRKHQKFTHFLPRPVPDPKVPELYKDIL  205

```


FIGURE 8

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1	MAPLAEVGGFLGGLGQQVGSFHLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH	59
		+ + + + + + + +	
Sbjct:	1	MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH	56
Query:	60	LHGILRRRLQLYCRTGFHLQILPDGSVQGTQRQDHSLSFGILEFISVAVGLVSIRGVDSGLYL	119
		+ + + +	
Sbjct:	57	LKGILRRRLQLYCRTGFHLEIFPNGTIQGTRKDHRSRFGILEFISIAVGLVSIRGVDSGLYL	116
Query:	120	GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA	179
		+ + + + +	
Sbjct:	117	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGT	176
Query:	180	RSKPHQKFTHFLPRPVDPERVPELYKDLL	208
		+ + + +	
Sbjct:	177	RTKRHQKFTHFLPRPVDPKVPELYKDIL	205

FIGURE 9

FGF-CX Query Length = 211
XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

Query:	1	MAPLAEVGGFLGGLEGLGQQVGSFHLPPAGERPPLLGERPSAAERSARGGPGAAQLAHL	60
		+ + + + + + +	
Sbjct:	1	MAPLADVGTFLGGYDALGQ-VGSFHLPPAKDSPLENDPLAQSERLSRSAP--SDLSHL	57
Query:	61	HGILRRRQLYCRTGFHLQILPDGVSQGTQDHSLFGILEFISVAVGLVSIPIGVDSGLYL	120
		+ + +	
Sbjct:	58	QGILRRRQLYCRTGFHLQILPDGNVQGTQDHSRFGILEFISVAIGLVSIPIGVDTGLYL	117
Query:	121	MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR	180
		+ + +	
Sbjct:	118	MNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGR	177
Query:	181	SKRHQKFTTHFLPRPVDPERVPELYKDLLMYT	211
		+ + + +	
Sbjct:	178	AKRHQKFTTHFLPRPVDPEKVPPELYKDLMGYS	208

FIGURE 10

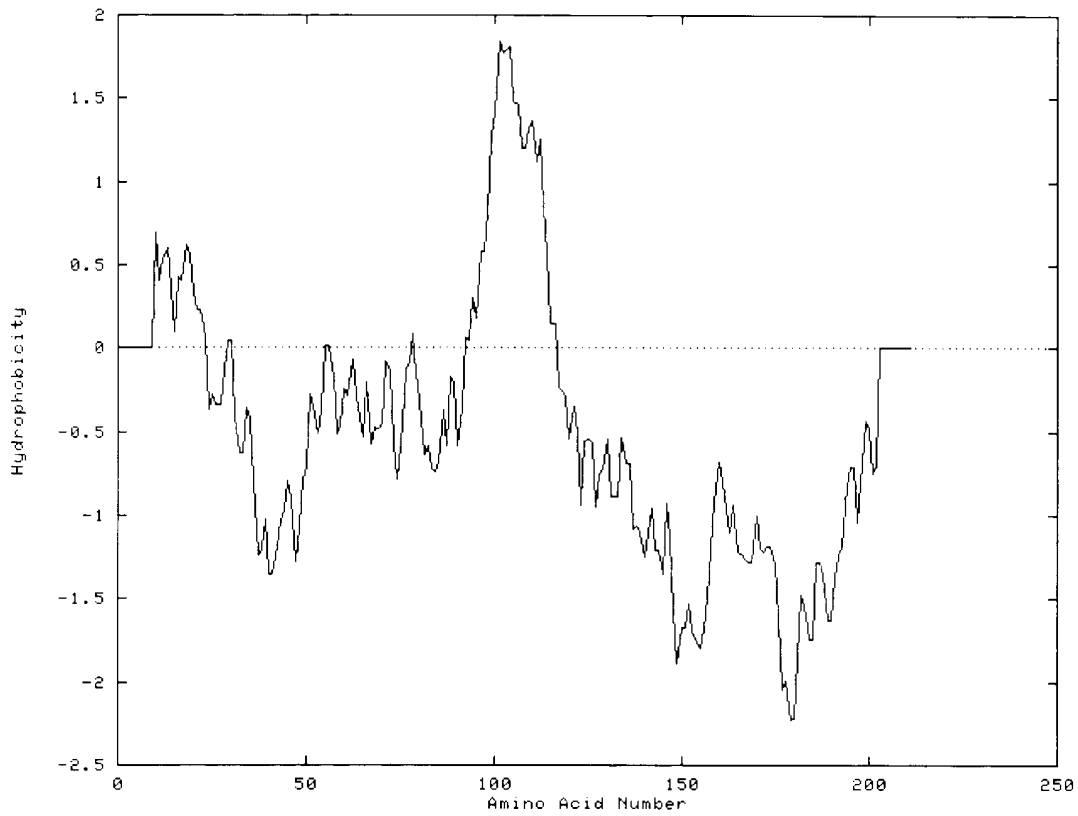
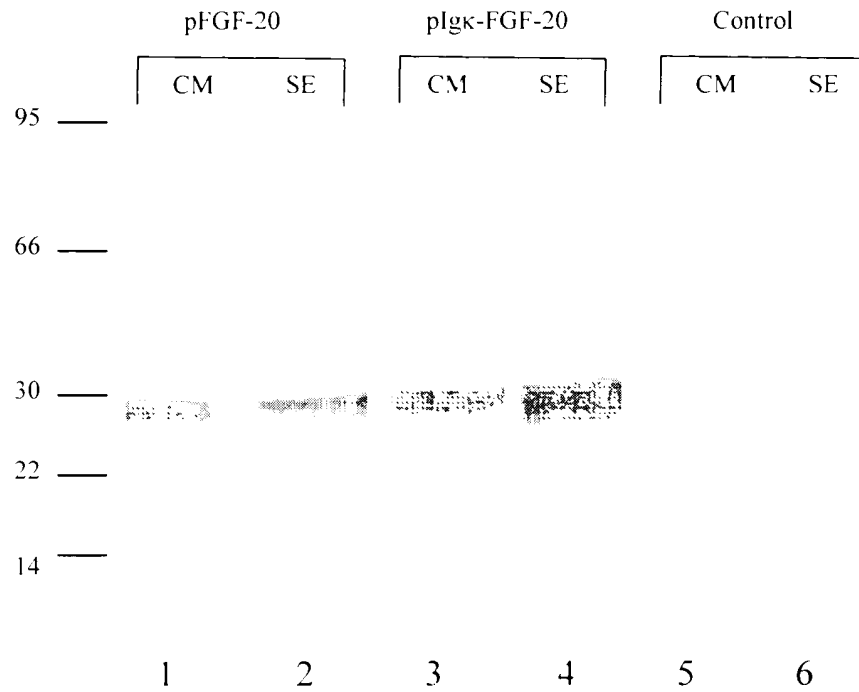


FIGURE 11

Panel A



Panel B

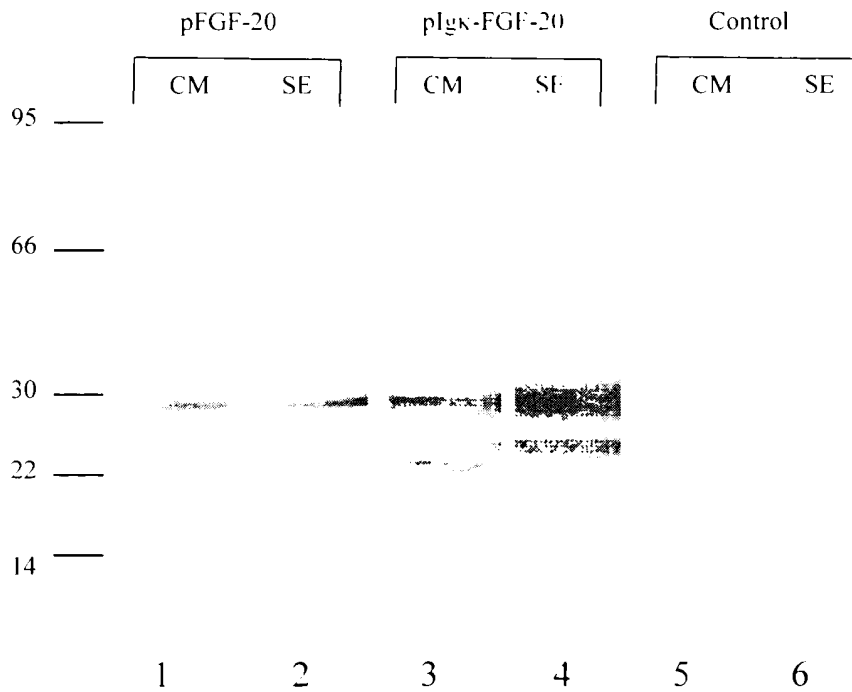


FIGURE 12.

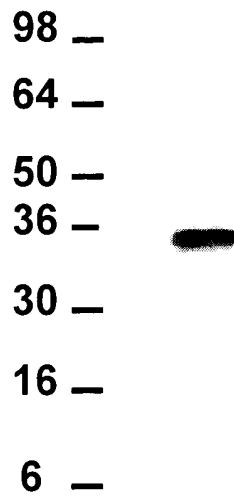


Figure 13.

Exon 1
...AGACAGTGAGAGCTCCCTGCCCATTTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGGCCTTAACT
TTTGGCGCTCGTTTTTGCTATAAATTTTCTCTATCCACCTCCATCCACCCCAACAACACTCTTTACTGGGGGGTCTTTT
GTGTTCCGGATCTCCCCCTCC**ATGG**CTCCCTTAGCCGAAGTGGGGGCTTTCTGGCGGCCTGGAGGGCTTGGGCCAGCA
M A P L A E V G G F L G G L E G L G Q Q
1
21 V G S H F L L P P A G E R P P L L G E R R S A A E R S
GGTGGGTTCGCATTTCCCTGTTCCTCCTGCCGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGGAGCGGA
48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T
GGTTCACCTGCAGATCCTGCCCCGACGGCAGCGGTGCAGGGCACCCGGCAGGACCCACAGCCTCTTCGGTATCTTGGAAATT
74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F
<-|-> **Exon 2**
CATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGTCTCTATCTTGGAAATGAATGACAAAGGAGAAC
101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L
<-|-> **Exon 3**
TCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTTCATCT
128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S
AACATATATAAACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAAACAAAGACGGAACTCCAAGAGATGGCGCCAG
154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R
GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCAGAAATTTGTACAAGGACC
181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L
TACTGATGTACACT**TGA**...
208 L M Y T

Figure 14.

98_

64_

50_

36_

30_

16_

6 _

Figure 15, Panel A.

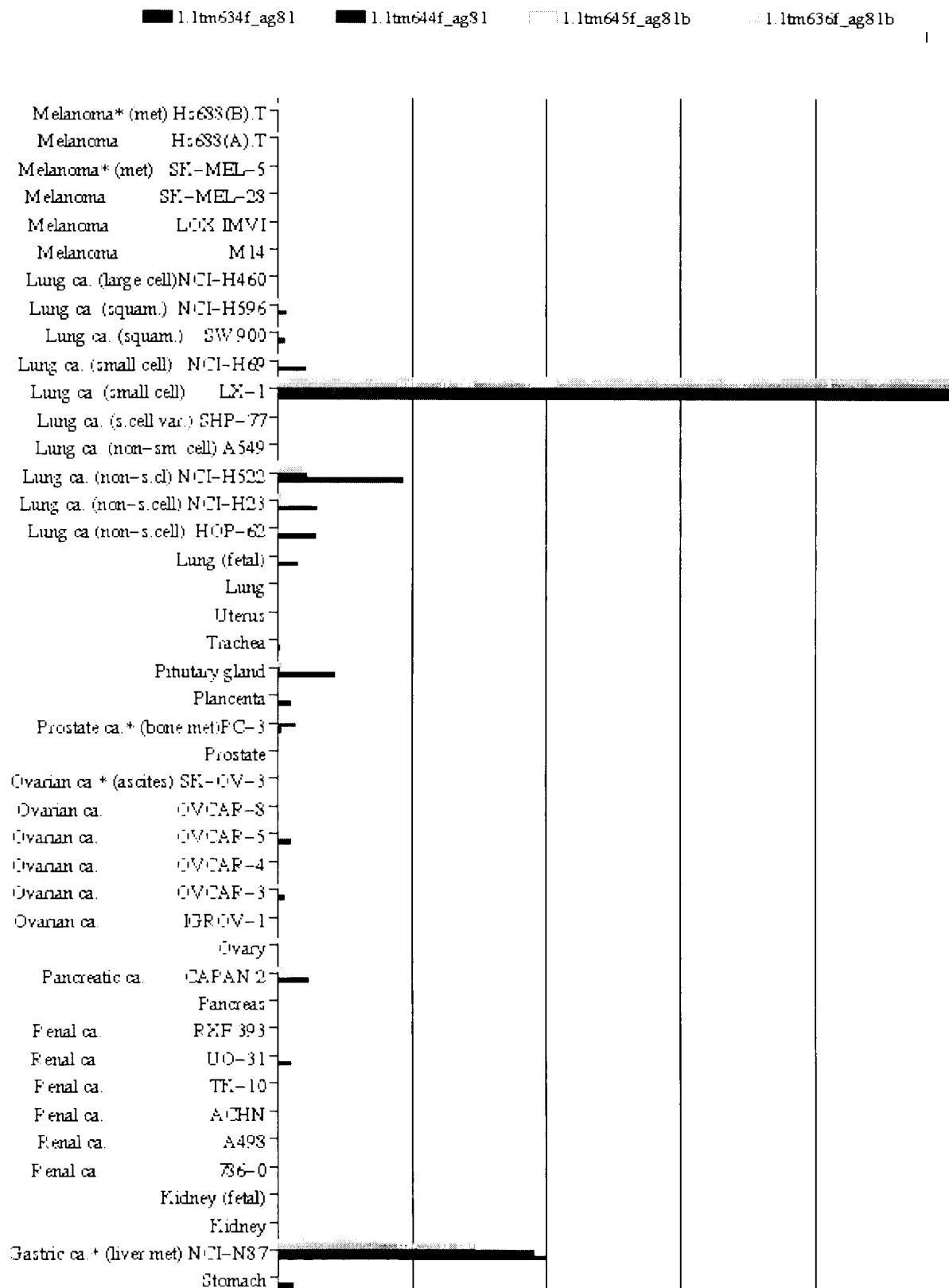


Figure 15, Panel B.

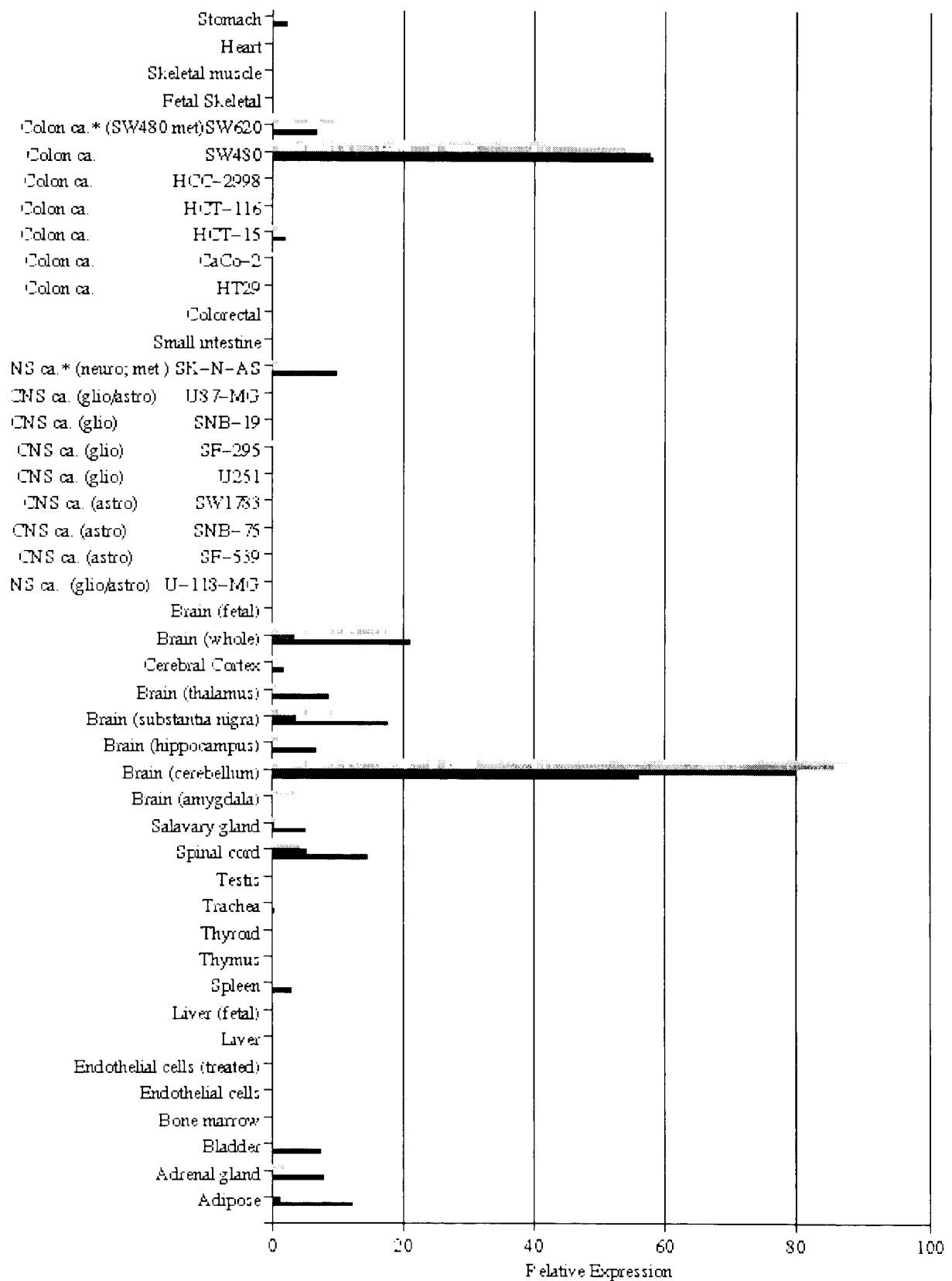


Figure 15, Panel C.

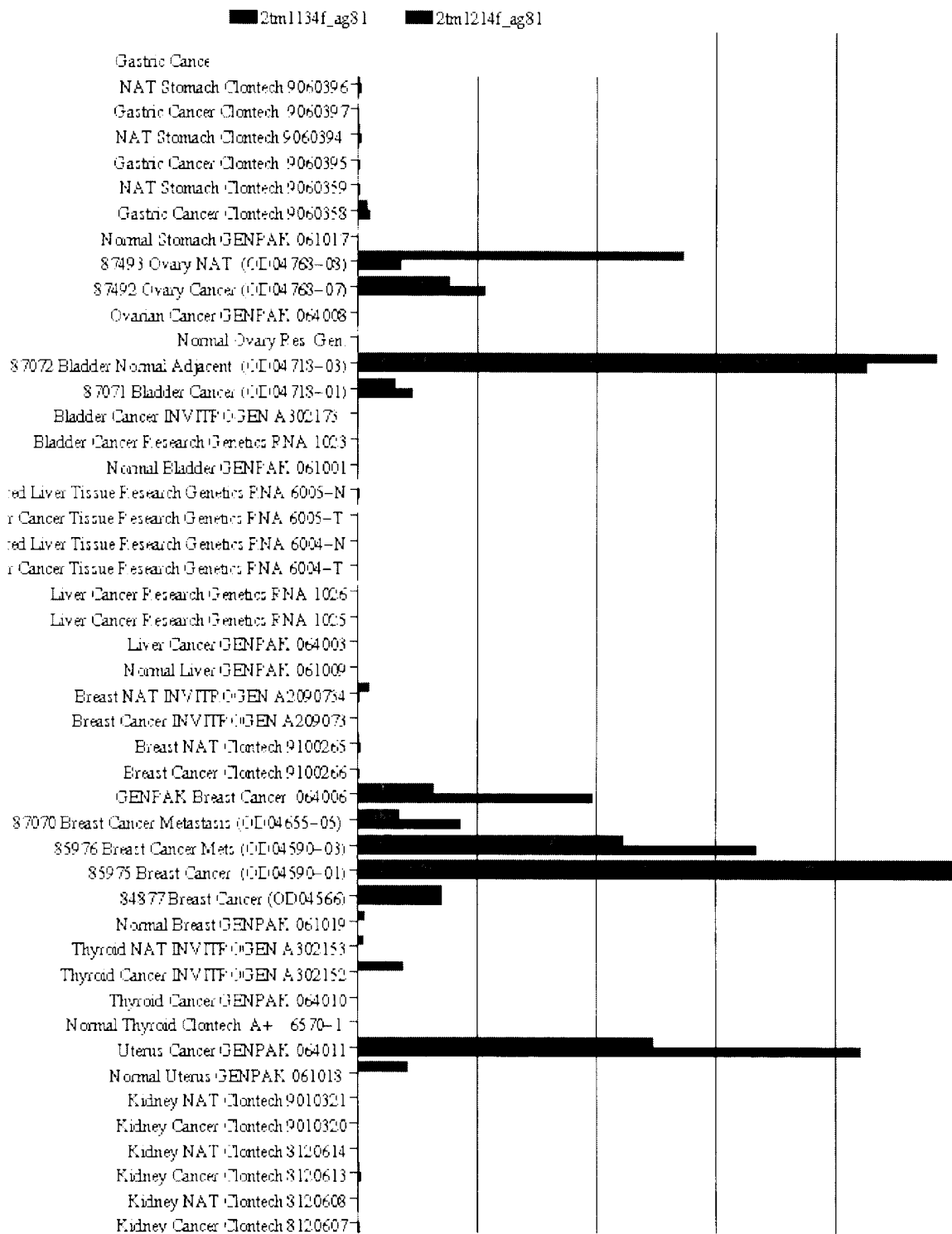


Figure 15, Panel D.

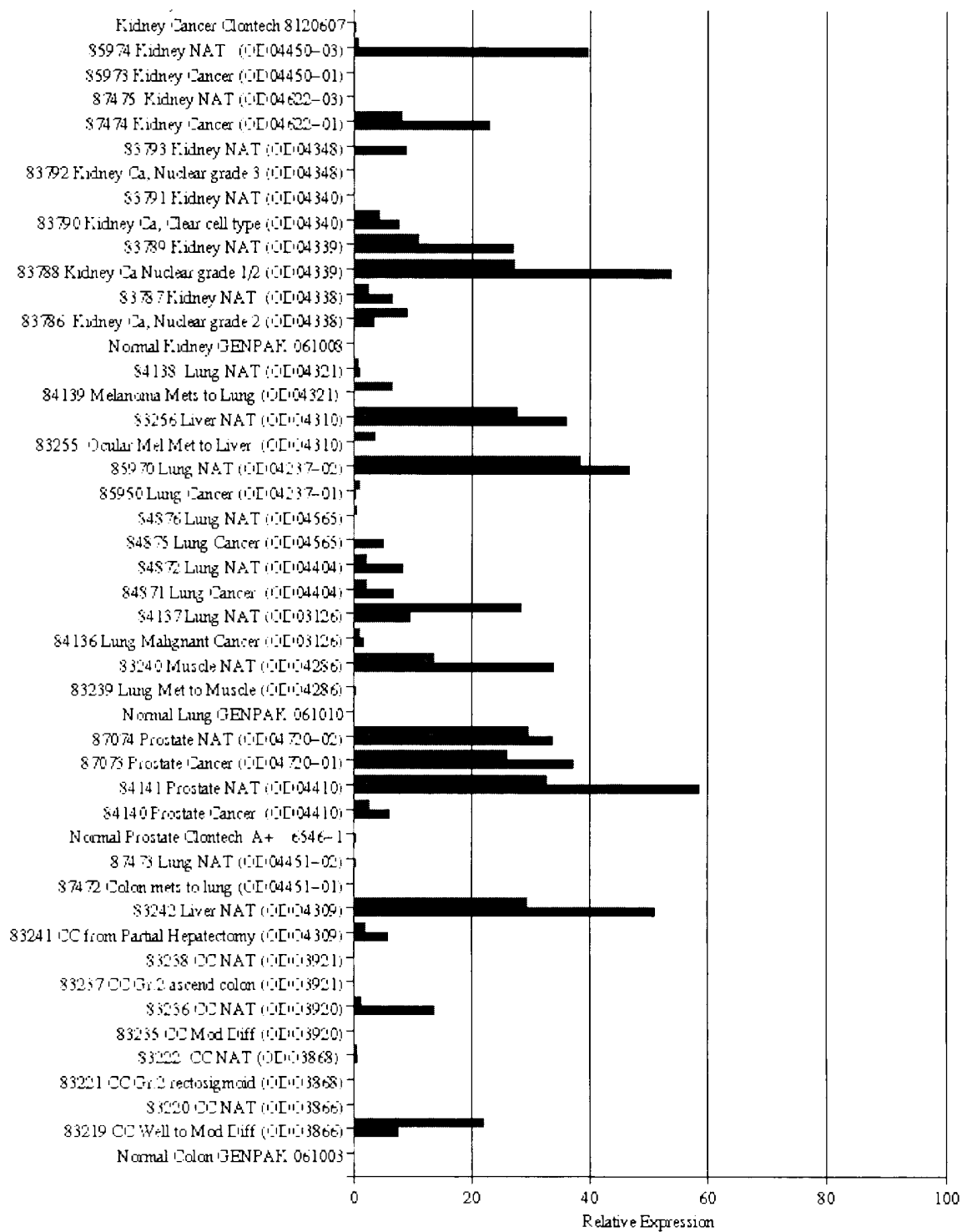


FIGURE 16.

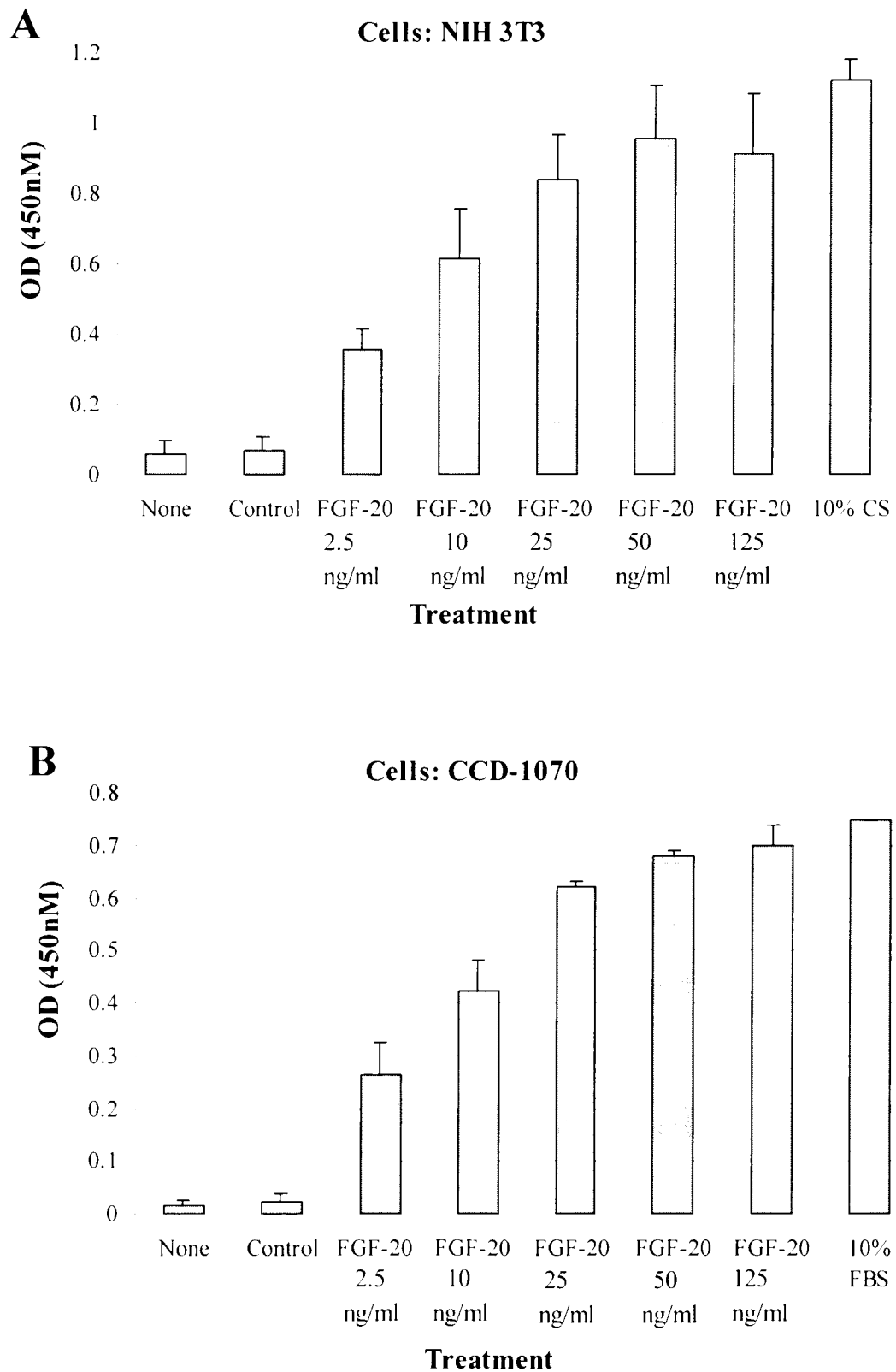


FIGURE 16 (continued).

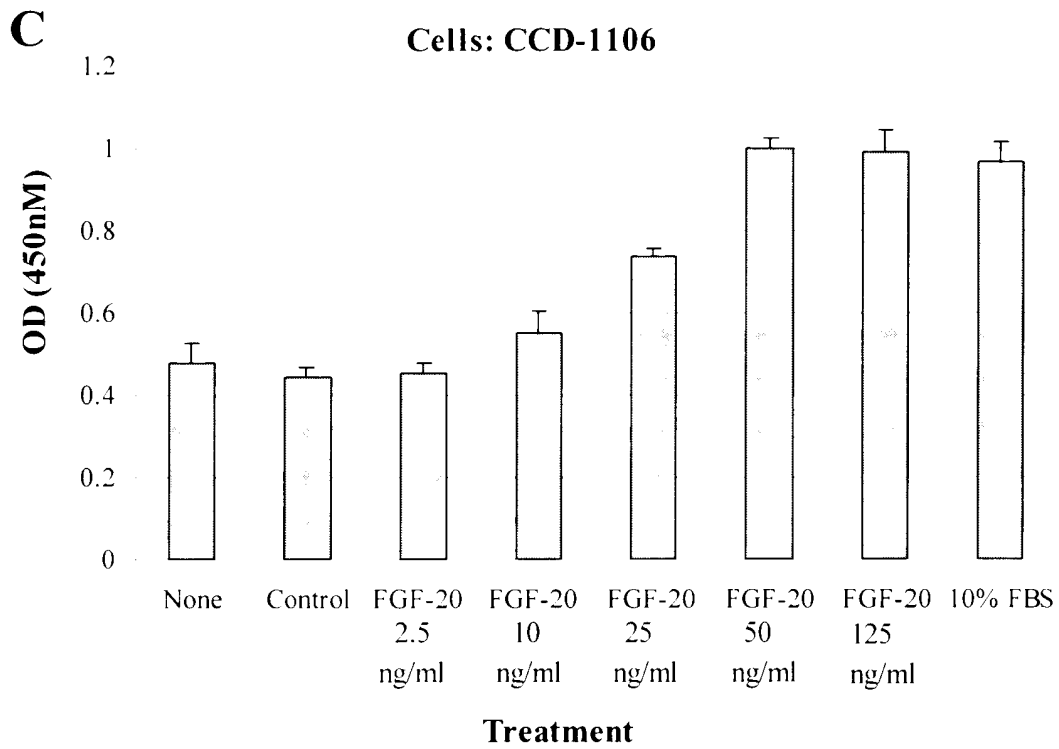


FIGURE 17.

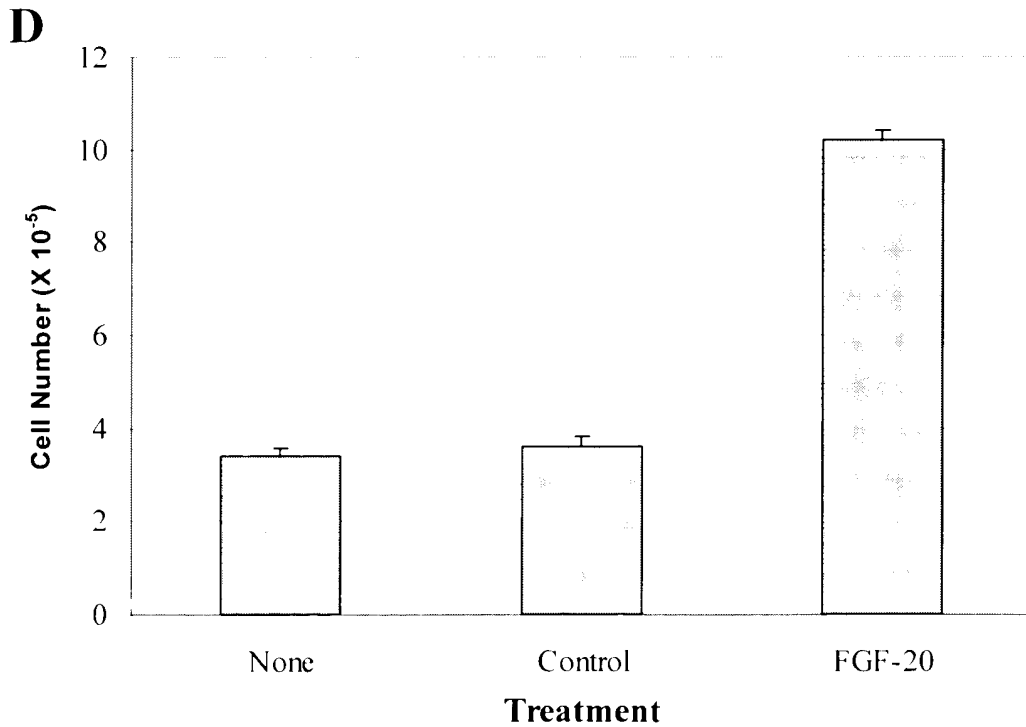


FIGURE 18.

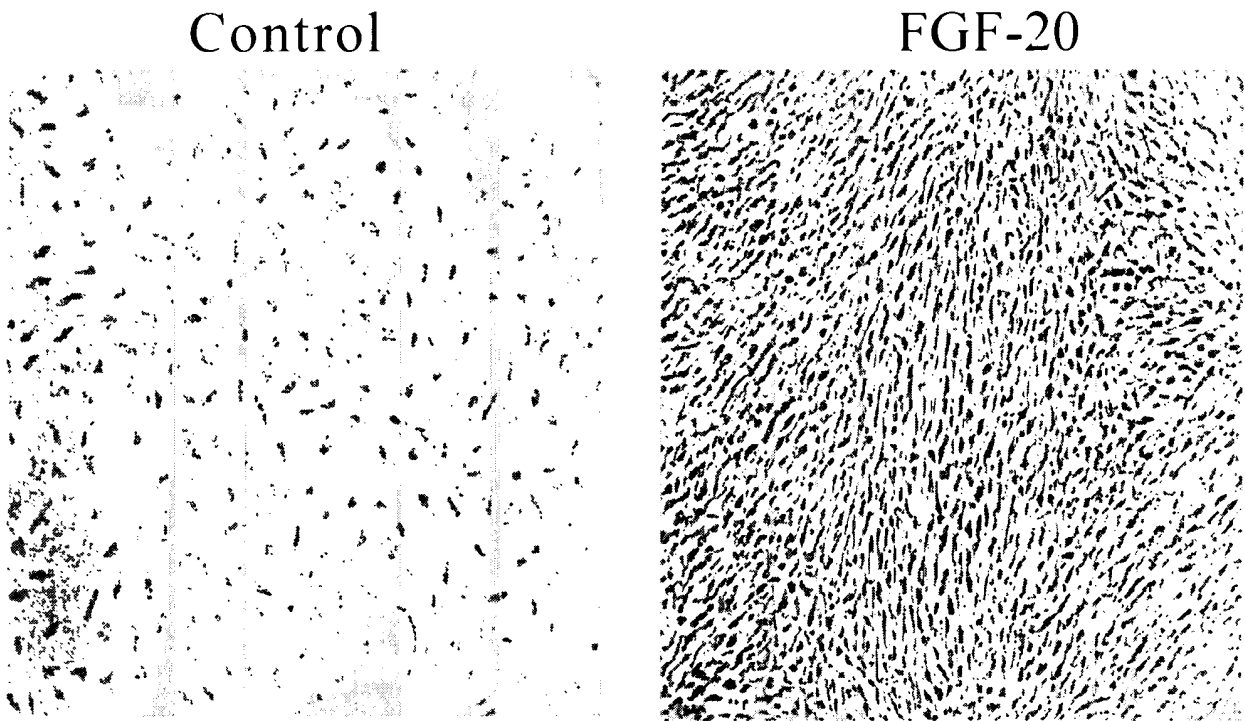


FIGURE 19.

TRADOCS.1

